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## RAW SEQUENCE LISTING

DATE: 10/19/2001

PATENT APPLICATION: US/09/972,268

TIME: 12:04:43

Input Set : A:\3101-A SEQ Listing.txt

Output Set: N:\CRF3\10192001\I972268.raw

3 <110> APPLICANT: Baum, Peter R.  
 4 Fanslow, William C.  
 5 Lofton, Timothy E.  
 6 Sorensen, Eric A.  
 7 Youakim, Adel  
 9 <120> TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND  
 USE THEREOF  
 11 <130> FILE REFERENCE: 3101-A  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/972,268 *OK*  
 14 <141> CURRENT FILING DATE: 2001-10-05  
 16 <150> PRIOR APPLICATION NUMBER: 60/238,557  
 17 <151> PRIOR FILING DATE: 2000-10-05  
 19 <160> NUMBER OF SEQ ID NOS: 39  
 21 <170> SOFTWARE: PatentIn version 3.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 3147  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(1626)  
 31 <223> OTHER INFORMATION:  
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 36 Ser Pro Leu Cys Pro Gly Gly Gly Lys Ala Gln Leu Ser Ser Ala Ser  
 37 1 5 10 15  
 39 ctc ctc gga gcc ggg ctc ctg ctg cag ccc ccg acg cca cct ccg ctg 96  
 40 Leu Leu Gly Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Pro Leu  
 41 20 25 30  
 43 ctg ctg ctg ctc ttc ccg ctg ctg ctc ttc tcc agg ctc tgt ggt gcc 144  
 44 Leu Leu Leu Phe Pro Leu Leu Phe Ser Arg Leu Cys Gly Ala  
 45 35 40 45  
 47 tta gct gga cca att att gtg gag cca cat gtc aca gca gta tgg gga 192  
 48 Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly  
 49 50 55 60  
 51 aag aat gtt tca tta aag tgt tta att gaa gta aat gaa acc ata aca 240  
 52 Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr  
 53 65 70 75 80  
 55 cag att tca tgg gag aag ata cat ggc aaa agt tca cag act gtt gca 288  
 56 Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala  
 57 85 90 95  
 59 gtt cac cat ccc caa tat gga ttc tct gtt caa gga gaa tat cag gga 336  
 60 Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly  
 61 100 105 110  
 63 aga gtc ttg ttt aaa aat tac tca ctt aat gat gca aca att act ctg 384  
 64 Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu  
 65 115 120 125  
 67 cat aac ata gga ttc tct gat tct gga aaa tac atc tgc aaa gct gtt 432

ENTERED

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68 His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val
69      130                      135                      140
71 aca ttc ccg ctt gga aat gcc cag tcc tct aca act gta act gtg tta      480
72 Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu
73 145                      150                      155                      160
75 gtt gaa ccc act gtg agc ctg ata aaa ggg cca gat tct tta att gat      528
76 Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp
77      165                      170                      175
79 gga gga aat gaa aca gta gca gcc att tgc atc gca gcc act gga aaa      576
80 Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys
81      180                      185                      190
83 ccc gtt gca cat att gac tgg gaa ggt gat ctt ggt gaa atg gaa tcc      624
84 Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser
85      195                      200                      205
87 act aca act tct ttt cca aat gaa acg gca acg att atc agc cag tac      672
88 Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr
89      210                      215                      220
91 aag cta ttt cca acc aga ttt gct aga gga agg cga att act tgt gtt      720
92 Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val
93 225                      230                      235                      240
95 gta aaa cat cca gcc ttg gaa aag gac atc cga tac tct ttc ata tta      768
96 Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu
97      245                      250                      255
99 gac ata cag tat gct cct gaa gtt tgc gta aca gga tat gat gga aat      816
100 Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn
101      260                      265                      270
103 tgg ttt gta gga aga aaa ggt gtt aat ctc aaa tgt aat gct gat gca      864
104 Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala
105      275                      280                      285
107 aat cca cca ccc ttc aaa tct gtg tgg agc agg ttg gat gga caa tgg      912
108 Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp
109      290                      295                      300
111 cct gat ggt tta ttg gct tca gac aat act ctt cat ttt gtc cat cca      960
112 Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro
113 305                      310                      315                      320
115 ttg act ttc aat tat tct ggt gtt tat atc tgt aaa gtg acc aat tcc      1008
116 Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser
117      325                      330                      335
119 ctt ggt caa aga agt gac caa aaa gtc atc tac att tca gat cct cct      1056
120 Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro
121      340                      345                      350
123 act act acc acc ctt cag cct aca att cag tgg cat ccc tca act gct      1104
124 Thr Thr Thr Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala
125      355                      360                      365
127 gac atc gag gat cta gca aca gaa cct aaa aaa ttg ccc ttc cca ttg      1152
128 Asp Ile Glu Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu
129      370                      375                      380
131 tca act ttg gca aca att aag gat gac aca att gcc acg atc att gct      1200
132 Ser Thr Leu Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala

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133 385          390          395          400
135 agt gta gtg ggt ggg gct ctc ttc ata gta ctt gta agt gtt ttg gct 1248
136 Ser Val Val Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala
137          405          410          415
139 gga ata ttc tgc tat agg aga aga cgg acg ttt cgt gga gac tac ttt 1296
140 Gly Ile Phe Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe
141          420          425          430
143 gcc aag aac tac att cca cca tca gat atg caa aaa gaa tca caa ata 1344
144 Ala Lys Asn Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile
145          435          440          445
147 gat gtt ctt caa caa gat gag ctt gat tct tac cca gac agt gta aaa 1392
148 Asp Val Leu Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys
149          450          455          460
151 aaa gaa aac aaa aat cca gtg aac aat cta ata cgt aaa gac tat tta 1440
152 Lys Glu Asn Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu
153 465          470          475          480
155 gaa gag cct gaa aaa act cag tgg aac aat gta gaa aat ctc aat agg 1488
156 Glu Glu Pro Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg
157          485          490          495
159 ttt gaa aga cca atg gat tat tat gaa gat cta aaa atg gga atg aag 1536
160 Phe Glu Arg Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys
161          500          505          510
163 ttt gtc agt gat gaa cat tat gat gaa aac gaa gat gac tta gtt tca 1584
164 Phe Val Ser Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser
165          515          520          525
167 cat gta gat ggt tcc gta att tcc agg agg gag tgg tat gtt 1626
168 His Val Asp Gly Ser Val Ile Ser Arg Arg Glu Trp Tyr Val
169          530          535          540
171 tagcaaccac tgaatgtgac ttaactatgt acaatgttca ttcacactag ttgatcattt 1686
173 tcagattgtt caactttttt cttgaggaag aataagcttt ttcaagttga ttttcaagct 1746
175 tactttttat attcctaactt gacaaatgaa aatgtaaaaat ctgagttcag tgtatctaag 1806
177 ctgctttaca attttttttt aatgctgtac tactgtctca agattttaaatt tttaatgcag 1866
179 agtactttat tgggtgtgagg cacacaggta agaagaaatg tcaacattaa atgtatgact 1926
181 tacttggtac aaaaattttt taaaaaggga actaccttga cattgtgtat taaatgttta 1986
183 cctaagacta taatctcaag tatgatgttt gttaacata tacctctcaa aatttatcac 2046
185 cactcaatga cactgcatca aaattgacta taaaactaat tcaagaaata tttatatata 2106
187 ttttttaata tacaaaaaat atttagcctg atggaatggc tttccttttc aaacattatt 2166
189 ttctaagttt ctatacaaat gaaatcttta cctctgcata ttaatgagcc ttgccataat 2226
191 tactgtagag tggcttttca aagataatttt gttgcactaa aactgttgta gtaaaactcag 2286
193 tgaacatgat gtgtggaaga gcataattag ctggtcaata tttttgtcca aaatacctgc 2346
195 aagagtaata aaatacatac ctttcaaaca tgataattat tagttttttt tttcctttct 2406
197 ggaacatgga ttttggtaca ttagcagtag ccttatttta atgctttatg tctaaacat 2466
199 actaatagaa atgaaaagac gcagagagag catttcggaa tactgaagta ctagttttag 2526
201 aaatgagact ttcagccaac aatctataga aagaatttta tggaccatct tgttttagtt 2586
203 atttaatggt gatgttggtc aaatgggtaa atgtacagaa agaaaatttt agagtaaact 2646
205 tggaactttg gatataacta gaaaaaacta gattatagaa ttagtcggtg acacttgcta 2706
207 atggacattg gcattcatct cctttttcct cctaagtgtg tgtatgtgtt ttaagatttc 2766
209 tgtttttacg attaaaactg gaaacatgag gttttttggt tttgtttttt tacataatta 2826
211 catatatattc ttctgaatca tttatctttt gagaaagaaa tgttacctaa acttcaaatg 2886

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213 tgctttttgt ttgtgaggta attaaattgc ttctaCagtg gaggcttaca aaattattgt 2946
215 gacaactatt ttgaagctga aaggatagtt tttctattgc taagtcattt gaaaaagtga 3006
217 ccatttttgcc agtgaaatga agtggaagtt agtaggagaa tcataaatta aatatattat 3066
219 tttgttaata aaaaggcaaa gtagtaggta ctttttaaac cctcccaacc agccctttct 3126
221 caatattcat caaatctaaa a 3147
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225 <211> LENGTH: 542
226 <212> TYPE: PRT
227 <213> ORGANISM: homo sapiens
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232 1 5 10 15
235 Leu Leu Gly Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Leu
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239 Leu Leu Leu Leu Phe Pro Leu Leu Leu Phe Ser Arg Leu Cys Gly Ala
240 35 40 45
243 Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly
244 50 55 60
247 Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr
248 65 70 75 80
251 Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala
252 85 90 95
255 Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly
256 100 105 110
259 Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu
260 115 120 125
263 His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val
264 130 135 140
267 Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu
268 145 150 155 160
271 Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp
272 165 170 175
275 Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys
276 180 185 190
279 Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser
280 195 200 205
283 Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr
284 210 215 220
287 Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val
288 225 230 235 240
291 Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu
292 245 250 255
295 Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn
296 260 265 270
299 Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala
300 275 280 285
303 Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp
304 290 295 300
307 Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro

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308 305          310          315          320
311 Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser
312          325          330          335
315 Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro
316          340          345          350
319 Thr Thr Thr Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala
320          355          360          365
323 Asp Ile Glu Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu
324          370          375          380
327 Ser Thr Leu Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala
328 385          390          395          400
331 Ser Val Val Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala
332          405          410          415
335 Gly Ile Phe Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe
336          420          425          430
339 Ala Lys Asn Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile
340          435          440          445
343 Asp Val Leu Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys
344          450          455          460
347 Lys Glu Asn Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu
348 465          470          475          480
351 Glu Glu Pro Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg
352          485          490          495
355 Phe Glu Arg Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys
356          500          505          510
359 Phe Val Ser Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser
360          515          520          525
363 His Val Asp Gly Ser Val Ile Ser Arg Arg Glu Trp Tyr Val
364          530          535          540

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367 &lt;210&gt; SEQ ID NO: 3

368 &lt;211&gt; LENGTH: 1650

369 &lt;212&gt; TYPE: DNA

370 &lt;213&gt; ORGANISM: Artificial Sequence ✓

372 &lt;220&gt; FEATURE:

373 <223> OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest  
are from

374 m human Nectin-3 alpha

376 &lt;220&gt; FEATURE:

377 &lt;221&gt; NAME/KEY: CDS

378 &lt;222&gt; LOCATION: (1)..(1650)

379 &lt;223&gt; OTHER INFORMATION: ✓

382 &lt;400&gt; SEQUENCE: 3

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385 1          5          10          15
387 gca caa ctt tcc tcc gct tct ctc ctc gga gcc ggg ctc ctg ctg cag      96
388 Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
389          20          25          30
391 ccc ccg acg cca cct ccg ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc      144
392 Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/972,268

DATE: 10/19/2001

TIME: 12:04:44

Input Set : A:\3101-A SEQ Listing.txt

Output Set: N:\CRF3\10192001\I972268.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number